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(2600 bp)

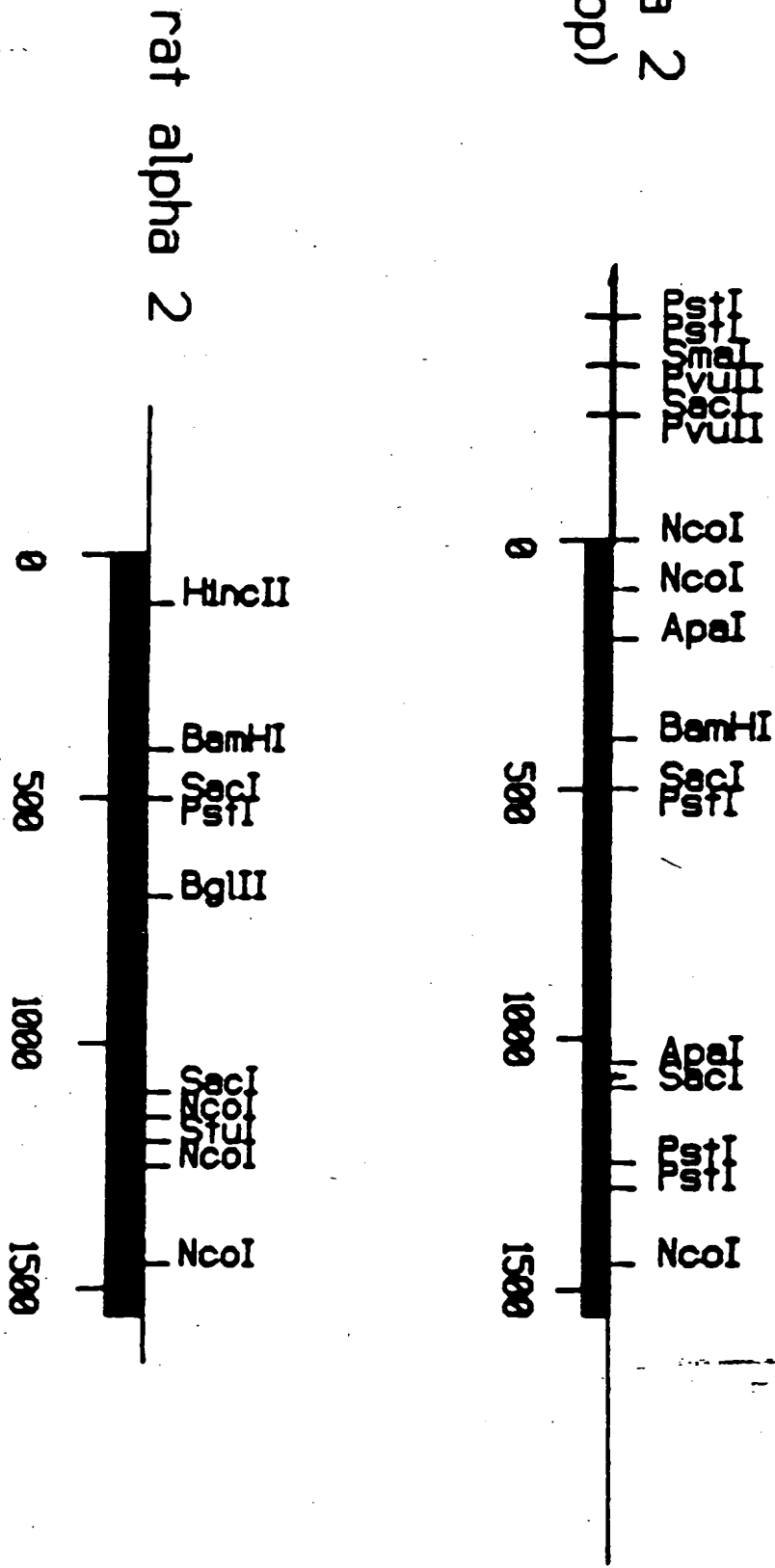


FIGURE 1

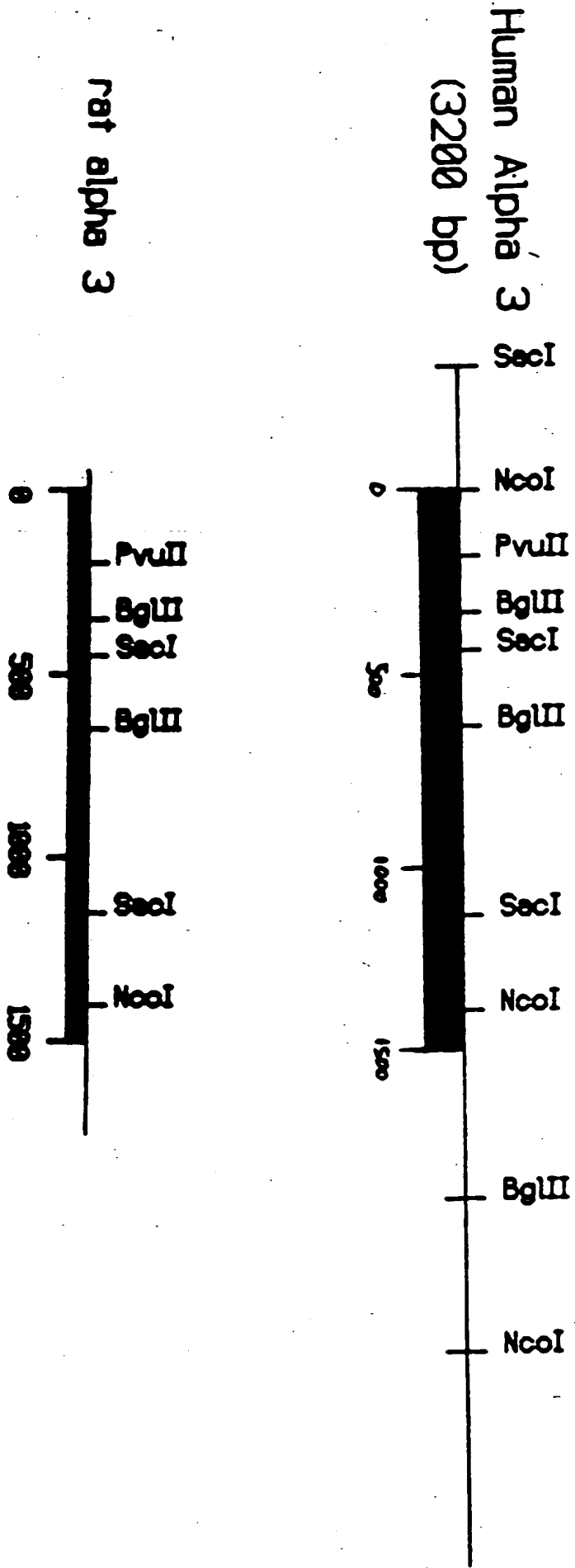


FIGURE 2

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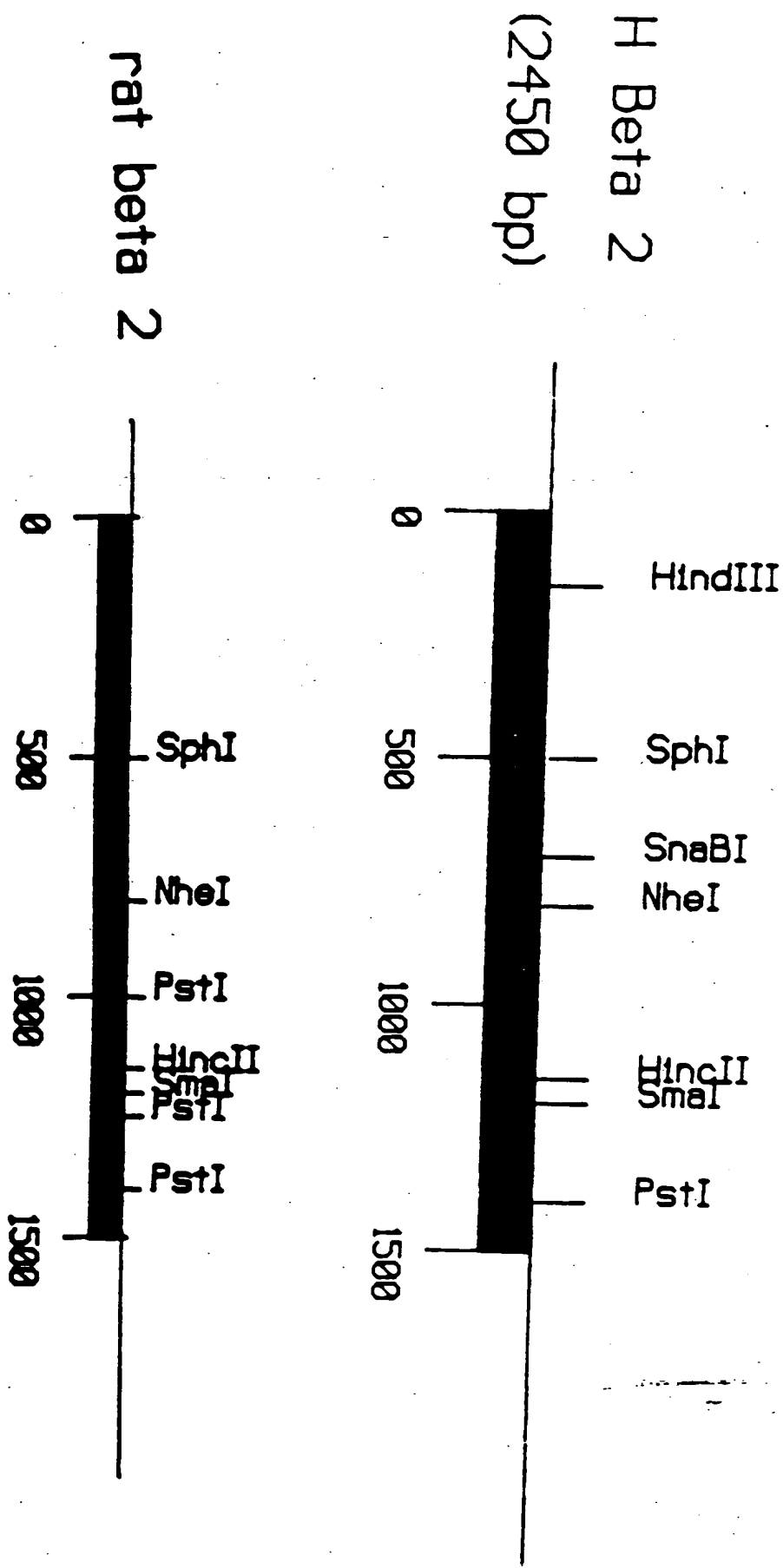


FIGURE 3

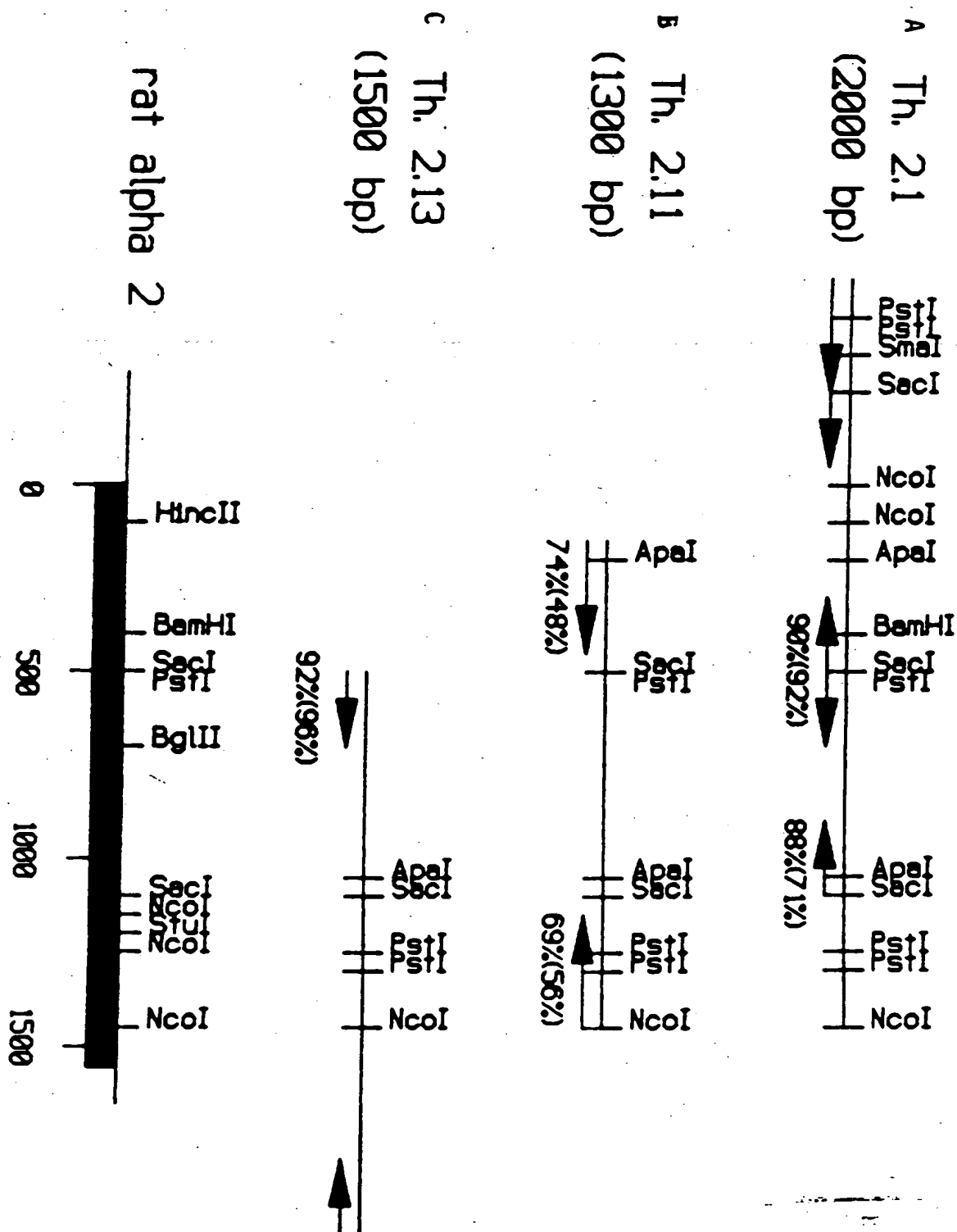


FIGURE 1

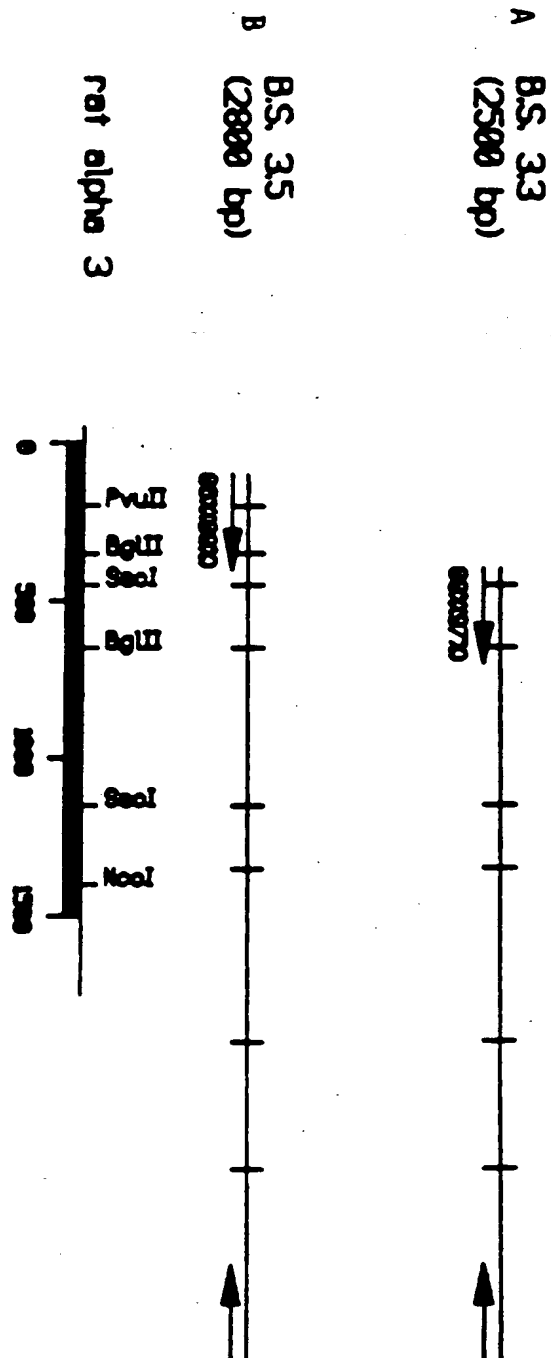


FIGURE 5

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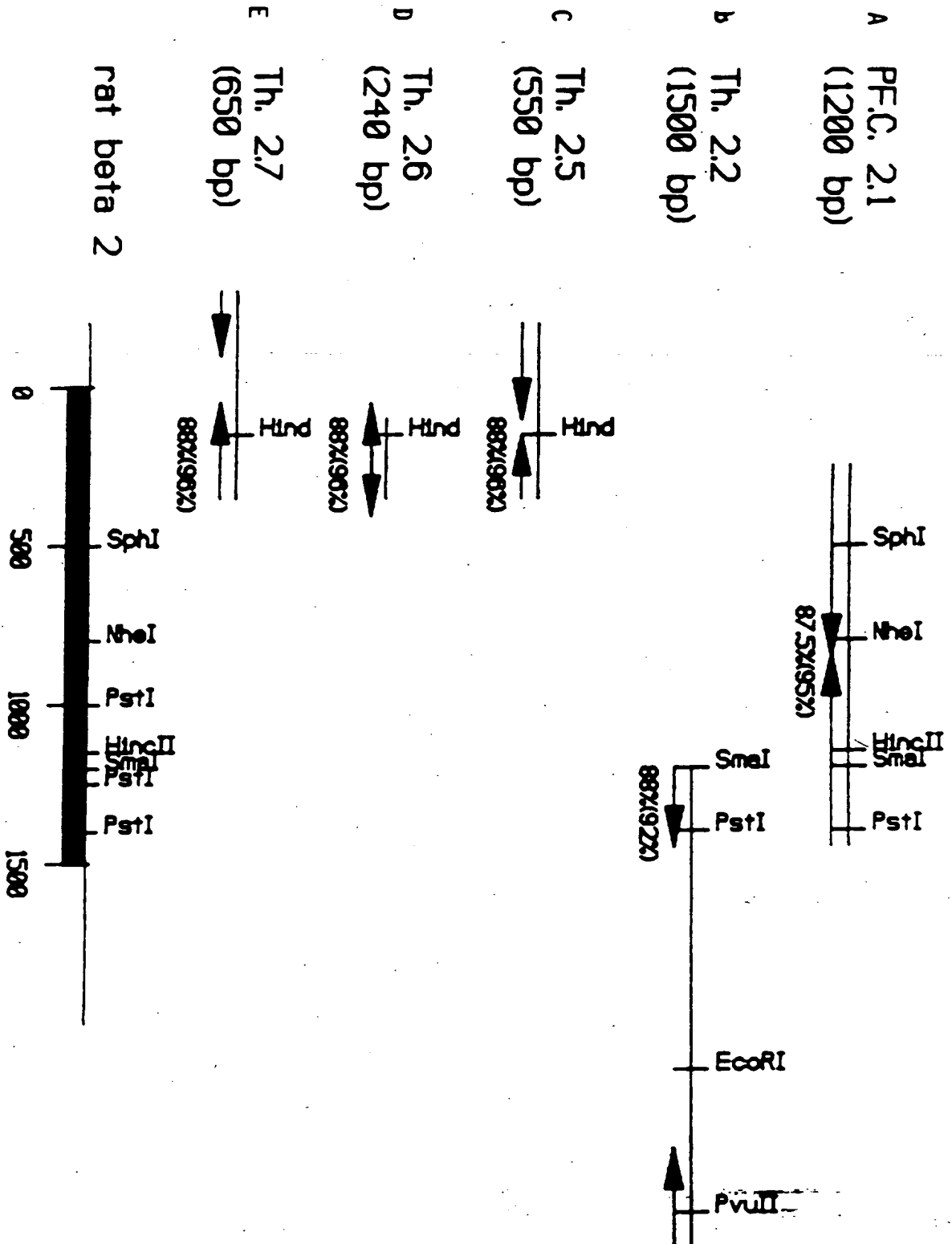


FIGURE 6

SECTION A

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195 .....GCTAAACAGGAGTGGAGCGACTACAACTGCGCTGGAAC 157
      || ||||| |||| ||||| ||||| ||||| ||||| |||||
251 CCAATGTCTGGCTAAAGCAGGAATGGAATGACTACAAGCTGCGCTGGGAC 300
156 CCCGCTGATTTTGGCAACATCACATCTCTCAGGGTCCCTTCTGAGATGAT 107
      || ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 CCCGCTGAGTTTGGCAATGTCACCTCCCTGCGCGTCCCTTCAGAGATGAT 350
      BaHI
106 CTGGATCCCGACATTGTTCTCTACAACA...AAATGGGGAGTTTGCAG 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
351 CTGGATCCAGACATTGTCCTCTACAACAATGCAGATGGGGAGTTTGCAG 400
      59 TGACCCACATGACCAAGGCCACCTCTTCTCCACGGGCACTGTGCACTGG 10
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
401 TGACCCACATGACCAAGGCTCACCTCTTCTTCACGGGCACTGTGCACTGG 450
      9 GTGCCCCC
      |||||
451 GTGCCCCCA

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SECTION B

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1 CCCCTTCGACCAGCAGAACTGCAAGATGAAGTTTGGCTCCTGGACTTATG 50
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
501 CCCCTTCGACCAGCAGAACTGCAAGATGAAGTTTGGCTCCTGGACATATG 550
51 ACAAGGCCAAGATCGACCTGGAGCAGATGGAGCAGACTGTGGACCTGAAG 100
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
551 ACAAGGCCAAGATCGATCTGGAGCAGATGGAGAGGACAGTGGACCTGAAG 600
101 GACTACTGGGAGAGCGGCGAGTGGGCCATCGTCAATGCCACGGGCACCTA 150
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
601 GACTACTGGGAGAGTGGCGAGTGGGCCATTATCAATGCCACCGGAACCTA 650
151 CAACAGCAAGAAGTACGACTGCTGCGCCGAGATCTACCCCGACGTCACCT 200
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
651 TAACAGTAAGAAGTACGACTGCTGCGCGGAGATCTACCCCGATGTCACCT 700
201 AG..... 202
      |
701 ACTACTTTGTGATCCGGCGGCTGCCGCTGTTCTATACCATCAACCTCATC 750

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FIGURE 7

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SECTION A

1 .....CTGGCAGCAGAGGCTGAGCACCGTCTATTTG 31  
51 GATGCTGCTGCCAGCGGCCAGTGCCTCAGAAGCTGAGCACCGCCTGTTC 100  
32 AGCGGCTGTTTGAAGATTACAATGAGATCATCCGGCCTGTAGCCAACGTG 81  
101 AGTACCTGTTCTGAAGATTACAACGAGATCATCCGGCCAGTGGCTAATGTG 150  
82 TCTGACCCAGTCATCATCCATTTCTGAGGTGTCCATGTCTCAGCTGGTGAA 131  
151 TCCCATCCAGTCATCATCCAGTTTGAGGTGTCCATGTCTCAGCTGGTGAA 200  
132 GGTGGATGAAGTAAACCGATCATGGAGACCAACCTGTGGCTCAAGCAA 181  
201 GGTGGATGAAGTAAACCGATCATGGAAACCAACCTGTGGCTGAAGCAA 250  
182 TCTGGAATGACTACAAGCTGAAGTGGAAACCCCTCTGACTATGGTGGGGCA 231  
251 TCTGGAATGACTACAAGCTGAAATGGAAACCCCTCTGACTACCAAGGGGTG 300  
232 GAGTTCATGCGTGTCCCTGCACAGAGATCTGGAAAGCCAGACATTGT... 278  
301 GAGTTCATGCGTGTCCCTGCAGAGAGATCTGGAAACCAGACATCGTACT 350

SECTION B

1 .....TTCCAGGTGGACGACAAGACCAAAGCCT 28  
351 GTACAACAACGCTGATGGGGATTTCAGGTGGATGACAAGACCAAAGCTC 400  
29 TACTCAAGTACACTGGGGACGTGACTTGGATACCTCCGGCCATCTTTAG 78  
401 TACTCAAGTACACAGGAGAAGTGACTTGGATCCCGCCGGCCATCTTTAG 450  
79 AGCTCTGTAAAATCGACGTGACCTACTTCCCGTTTGATTACCAAAACTG 128  
451 AGCTCATGCAAAATCGACGTGACCTACTTCCCATTCGACTACCAAAACTG 500  
129 TACCATGAAGTTCGGTTCCTGGTCCTACGATAAGGCGAAAATCGATCTGG 178  
501 CACCATGAAGTTCGGCTCCTGGTCCTACGACAAGGCAAAGATCGACCTGG 550  
179 TCCTGATCGGCTCTTCCATGAACCTCAAGGACTATTGGGAGAGCGGCGAG 228  
551 TCCTCATCGGCTCCTCCATGAACCTCAAGGACTACTGGGAGAGTGGCGAG 600  
229 TGGGCCATCATCAAAGCCCCAGGCTACAAACACGACATCAAGTACAAGT 278  
601 TGGGCTATCATTAAAGCCCCGGGCTACAAACATGAAATCAAGTACAAGT 650  
279 CTGCGAGGAGATCTACCCCGACATCAC..... 305  
651 CTGTGAGGAGATCTACCAAGACATCACGTAATCGCTGTACATCCGTGCGC 700



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1  ATGCCCGCTGGCATGGCCGGCGCTGCGGCCCGTGGCGCTGCTCCTTGG 50
   |||| ||| |||||||| ||| || | | |||||||| |
1  ATGCTGGCTTGTCATGGCCGGGCACTCCAACCTCAATGGCGCTGTTC...AG 47

51  CTTGCGCCTCCTCCGGCTGTGCTCAGGGGTGTGGGGTACGGATACAGAGG 100
   |||| |||| || |||||||||||||| ||| || || |||||||
48  CTTCAGCCTTCTTTGGCTGTGCTCAGGGGTTTGGGAAGTACACAGAGG 97

101 AGCGGCTGGTGGAGCATCTCCTGGATCCTTCCCGCTACAACAAGCTTATC 150
     |||||| |||||||||| || |||| |||||| |||||| ||
98  AGCGGCTAGTGGAGCATCTCTTAGATCCCTCCCGCTATAACAAGCTGATT 147

151 CGCCAGCCACCAATGGCTCTGAGCTGGTGACAGTACAGCTTATGGTGTC 200
     || |||| || || |||||||||||||| |||||| |||| ||
148 CGTCCAGCTACTAACGGCTCTGAGCTGGTGACTGTACAGCTCATGGTATC 197

201 ACTGGCCAGCTCATCAGTGTGCATGAGCGGGAGCAGATCATGACCACCA 250
     |||| |||||| |||||| |||||| |||||| |||||| ||
198 ATTGGCTCAGCTCATTAGTGTGCACGAGCGGGAGCAGATCATGACCACCA 247

251 ATGTCTGGCTGACCCAGGAGTGGGAAGATTATCGCCTCACCTGGAAGCCT 300
     |||||| |||||| |||||| |||||| |||||| |||||| ||
248 ATGTCTGGCTGACCCAGGAGTGGGAAGATTACCGCCTCACATGGAAGCCT 297

301 GAAGAGTTTGACAACATGAAGAAAGTTCGGCTCCCTTCCAAACACATCTG 350
     || || || |||| |||||| |||||| |||||| |||||| ||
298 GAGGACTTCGACAATATGAAGAAAGTCCGGCTCCCTTCCAAACACATCTG 347

351 GCTCCAGATGTGGTCTGTACAACAATGCTGACGGCATGTACGAGGTGT 400
     |||||| |||| || |||||| |||||| |||||| |||| |
348 GCTCCAGATGTGGTCTTATACAACAATGCTGACGGCATGTACGAAGTCT 397

401 CCTTCTATTCCAATGCCGTGGTCTCCTATGATGGCAGCATCTTCTGGCTG 450
     |||||| |||||| |||||| |||||| |||||| |||| |
398 CCTTCTATTCCAATGCTGTGGTCTCCTATGATGGCAGCATCTTTTGGCTA 447
                                     Spri
451 CCGCCTGCCATCTACAAGAGTGCATGCAAGATTGAAGTAAAGCACTTCCC 500
     || |||||| |||||| |||||| |||||| || |||||| ||
448 CCACCTGCCATCTACAAGAGTGCATGCAAGATTGAGGTGAAGCACTTCCC 497

501 ATTTGACCAGCAGAACTGCACCATGAAGTTCGGTTCGTGGACCTACGACC 550
     |||||| |||||| |||||| || || || |||||| ||
498 ATTTGACCAGCAGAAATTGCACCATGAAGTTTCGCTCATGGACCTACGACC 547

551 GCACAGAGATCGACTTGGTGCTGAAGAGTGAGGTGGCCAGCCTGGACGAC 600
     | || |||| || |||||| || |||| |||||| |||| |
548 GTA CTGAGATTGACCTGGTGCTCAAAAGTGATGTGGCCAGTCTGGATGAC 597

601 TTCACACCTAGTGGTGAGTGGGACATCGTGGCGCTGCCGGGGCCGGGCAA 650
     |||||| || || |||||| || || |||| |||| |||| |
598 TTCACACCCAGCCGGGAGTGGGACATCATCGCACTGCCAGGGCCGACGCAA 647

651 CGAGAACCCCGACGACTCTACGTACGTGGACATCACGTATGACTTCATCA 700
     |||||| |||||| || || |||||| |||||| |||||| ||
648 CGAGAACCCAGACGACTCCACCTATGTGGACATCACCTATGACTTCATCA 697

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FIGURE 9(a)

701 TTCGCCGCAAGCCGCTCTTCTACACCATCAACCTCATCATCCCCTGTGTG 750  
 699 TTCGTCGCAAAACCACTCTTCTACACTATCAACCTCATCATCCCCTGCGTA 747  
 751 CTCATCACCTCGCTAGCCATCCTTGTCTTCTACCTGCCATCCGACTGTGG 800  
 748 CTCATCACCTCGCTGGCCATCCTGGTCTTCTACCTGCCCTCAGACTGTGG 797  
 801 CGAGAAGATGACGTTGTGCATCTCAGTGCTGCTGGCGCTCACGGTCTTCC 850  
 798 TGAAAAGATGACACTTTGTATTTCTGTGCTGCTAGCACTCACGGTGTTC 847  
 851 TGCTGCTCATCTCCAAGATCGTGCCCTCCACCTCCCTCGACGTGCCGCTC 900  
 848 TGCTGCTCATCTCCAAGATTGTGCCTCCACCTCCCTCGATGTACCGCTG 897  
 901 GTGGGCAAGTACCTCATGTTACCATGGTGCTTGTACCTTCTCCATCGT 950  
 898 GTGGGCAAGTACCTCATGTTTACCATGGTGCTAGTCACCTTCTCCATCGT 947  
 951 CACCAGCGTGTGCGTGCTCAACGTGCACCACCGCTCGCCCACCACGCACA 1000  
 948 CACCAGCGTGTGCTGCTCAATGTGCACCACCGCTCGCCTACCACGCACA 997  
 1001 CCATGGCCGCCCTGGGTGAAGGTGCTCTTCTTGGAGAAGCTGCCCGCGCTG 1050  
 998 CCATGGCCGCCCTGGGTCAAGGTGGTCTTCTTGGAGAAGCTGCCCACCTG 1047  
 1051 CTCTTCATGCAGCAGCCACGCCATCATTGCGCCCGTCAGCGCCTGCGCCT 1100  
 1048 CTCTTCTGTCAGCAGCCACGCCACCGCTGTGCACGTGAGCGTCTGCGCTT 1097  
 1101 GCGGCGACGCCAGCGTGAGCGCGAGGGCGCTGGAGCCCTCTTCTTCCGCG 1150  
 1099 GAGGAGGCGCCAGCGAGAGCGTGAGGGC...GAGGCGGTTTTCTTCCGTG 1144  
 1151 AAGCCCCAGGGGCCGACTCCTGCACGTGCTTCGTCAACCGCGCGTCGGTG 1200  
 1145 AAGGTCTTGCGGCTGACCCATGTACCTGCTTTGTCAACCCTGCATCAGTG 1194  
 1201 CAGGGGTGCGCCGGGGCCTTCGGGGCTGAGCCTGCACCAAGTGCGGGGCC 1250  
 1195 CAGGGCTTGGCTGGGGCTTTCGAGCTGAGCCCACTGCA...GCCGGGCC 1241  
 1251 CGGGCGCTCAGGGGAGCCGTGTGGCTGTGGCCTCCGGGAGGCGGTGGACG 1300  
 1242 GGGGCGCTCTGTGGGGCCATGCAGCTGTGGCCTCCGGGAAGCAGTGGATG 1291  
 1301 GCGTGCGCTTCATCGCAGACCACATGCGGAGCGAGGACGATGACCAGAGC 1350  
 1292 GCGTACGCTTCATTGCGGACCACATGCGAAGTGAGGATGATGACCAGAGT 1341  
 1351 GTGAGTGAGGACTGGAAGTACGTGCGCCATGCTGATCGACCGCCTCTTCT 1400  
 1342 GTGAGGGAGGACTGGAATACGTTGCCATGGTGATCGACCGCCTGTTCT 1391

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1401 CTGGATCTTTGTCTTTGTCTGTGTCTTTGGCACCATCGGCATGTTCTGC 1450  
|||||  
1392 GTGGATCTTTGTCTTTGTCTGTGTCTTTGGGACCGTCGGCATGTTCTGC 1441  
1451 AGCTCTCTTCCAGAACTACACCACCACCACCTTCCTCCACTCAGACCAC 1500  
|||||  
1442 AGCCTCTCTTCCAGAACTACACTGCCACTACCTTCCTCCACCCTGACCAC 1491  
1501 TCAGCCCCCAGCTCCAAGTGA 1521  
|||||  
1492 TCAGCTCCCAGCTCCAAGTGA 1512

FIGURE 9(c)